RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: _10/590,953_

Source: _1FWP_

Date Processed by STIC: _9/5/06_

ENTERED

IFW ρ

```
        RAW SEQUENCE LISTING              DATE: 09/05/2006
        PATENT APPLICATION:  US/10/590,953   TIME: 15:07:20

        Input Set : E:\PC32099A_SEQUENCE LISTING.txt
        Output Set: N:\CRF4\09052006\J590953.raw

     3 <110> APPLICANT: Pfizer Inc.; Pfizer Japan Inc.(for Japan)
     5 <120> TITLE OF INVENTION: GPR35
     7 <130> FILE REFERENCE: PC32099
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/590,953
C--> 9 <141> CURRENT FILING DATE: 2006-08-28
     9 <160> NUMBER OF SEQ ID NOS: 23
    11 <170> SOFTWARE: PatentIn version 3.1
    13 <210> SEQ ID NO: 1
    14 <211> LENGTH: 921
    15 <212> TYPE: DNA
    16 <213> ORGANISM: rat
    18 <400> SEQUENCE: 1
    19 atgaacaata caaattgtag catcctcccg tggcctgctg cagtcaacca catcttcacc   60
    21 atctacttgg tcttgctgct ggtgctgggc ctgctgctca atggcctggc actctgggta  120
    23 ttctgctatc gcatgcacca gtggacggag acccgagtct atatgaccaa cctggctgtg  180
    25 gctgacgtct gcctgctctg ctccttgcca ttcgtgctgt actccctgaa atacagtact  240
    27 tcggacacac ccatctgcca gctctcacag ggcatctacc tggtcaacag gtacatgagc  300
    29 ataagcttgg tcaccgccat tgctgtggac cgctatgtgg cagtgcggca tcccctgcgt  360
    31 gcccgtgagc tgcggtcccc acggcaggct ggagcagtgt gtgtggccct ctgggtgata  420
    33 gtggtcacct ccctggtact gcgctggcgc ctggggatac aggagggtgg cttctgcttc  480
    35 agcagccaaa atcggtacaa cttcagcacc actgccttct cgctgctggg attctacctg  540
    37 ccgctggcca tagtggtctt ctgctctttg caggttgtga ctgcgttggc ccgaaggcca  600
    39 gccactgacg tggagcaggt ggaggccact cagaaggcca cccgcatggt ctgggccaac  660
    41 ttggccgtgt ttatcatctg cttcctgccc ctgcatttga tcctgacagt gcaggtctcc  720
    43 ctgaacctcc acacctgcgc tgcccgaaac atcttcagcc gtgccctgac aatcacagcc  780
    45 aagctctcag acatcaactg ctgcctggat gccatctgtt actactacat ggccaaagag  840
    47 ttccaggatg cgtccttgcg ggccacagcc tctagcacac cccacaagag ccaagatact  900
    49 cagagcctga gcctcaccta g                                           921
    52 <210> SEQ ID NO: 2
    53 <211> LENGTH: 306
    54 <212> TYPE: PRT
    55 <213> ORGANISM: rat
    57 <400> SEQUENCE: 2
    59 Met Asn Asn Thr Asn Cys Ser Ile Leu Pro Trp Pro Ala Ala Val Asn
    60 1               5                   10                  15
    63 His Ile Phe Thr Ile Tyr Leu Val Leu Leu Leu Val Leu Gly Leu Leu
    64              20                  25                  30
    67 Leu Asn Gly Leu Ala Leu Trp Val Phe Cys Tyr Arg Met His Gln Trp
    68          35                  40                  45
    71 Thr Glu Thr Arg Val Tyr Met Thr Asn Leu Ala Val Ala Asp Val Cys
    72      50                  55                  60
    75 Leu Leu Cys Ser Leu Pro Phe Val Leu Tyr Ser Leu Lys Tyr Ser Thr
    76 65                  70                  75                  80
```

```
 79 Ser Asp Thr Pro Ile Cys Gln Leu Ser Gln Gly Ile Tyr Leu Val Asn
 80                 85                  90                  95
 83 Arg Tyr Met Ser Ile Ser Leu Val Thr Ala Ile Ala Val Asp Arg Tyr
 84             100                 105                 110
 87 Val Ala Val Arg His Pro Leu Arg Ala Arg Glu Leu Arg Ser Pro Arg
 88         115                 120                 125
 91 Gln Ala Gly Ala Val Cys Val Ala Leu Trp Val Ile Val Val Thr Ser
 92     130                 135                 140
 95 Leu Val Leu Arg Trp Arg Leu Gly Ile Gln Glu Gly Gly Phe Cys Phe
 96 145                 150                 155                 160
 99 Ser Ser Gln Asn Arg Tyr Asn Phe Ser Thr Thr Ala Phe Ser Leu Leu
100                 165                 170                 175
103 Gly Phe Tyr Leu Pro Leu Ala Ile Val Val Phe Cys Ser Leu Gln Val
104             180                 185                 190
107 Val Thr Ala Leu Ala Arg Arg Pro Ala Thr Asp Val Glu Gln Val Glu
108         195                 200                 205
111 Ala Thr Gln Lys Ala Thr Arg Met Val Trp Ala Asn Leu Ala Val Phe
112     210                 215                 220
115 Ile Ile Cys Phe Leu Pro Leu His Leu Ile Leu Thr Val Gln Val Ser
116 225                 230                 235                 240
119 Leu Asn Leu His Thr Cys Ala Ala Arg Asn Ile Phe Ser Arg Ala Leu
120                 245                 250                 255
123 Thr Ile Thr Ala Lys Leu Ser Asp Ile Asn Cys Cys Leu Asp Ala Ile
124             260                 265                 270
127 Cys Tyr Tyr Tyr Met Ala Lys Glu Phe Gln Asp Ala Ser Leu Arg Ala
128             275                 280                 285
131 Thr Ala Ser Ser Thr Pro His Lys Ser Gln Asp Thr Gln Ser Leu Ser
132     290                 295                 300
135 Leu Thr
136 305
139 <210> SEQ ID NO: 3
140 <211> LENGTH: 930
141 <212> TYPE: DNA
142 <213> ORGANISM: human
144 <400> SEQUENCE: 3
145 atgaatggca cctacaacac ctgtggctcc agcgacctca cctggccccc agcgatcaag      60
147 ctgggcttct acgcctactt gggcgtcctg ctggtgctag gcctgctgct caacagcctg     120
149 gcgctctggg tgttctgctg ccgcatgcag cagtggacgg agaccgcat ctacatgacc      180
151 aacctggcgg tggccgacct ctgcctgctg tgcaccttgc ccttcgtgct gcactccctg     240
153 cgagacacct cagacacgcc gctgtgccag ctctcccagg gcatctacct gaccaacagg     300
155 tacatgagca tcagcctggt catggccatc gccgtggacc gctatgtggc cgtgcggcac     360
157 ccgctgcgtg cccgcgggct gcggtccccc aggcaggctg cggccgtgtg cgcggtcctc     420
159 tgggtgctgg tcatcggctc cctggtggct cgctggctcc tggggattca ggagggcggc     480
161 ttctgcttca ggagcacccg gcacaatttc aactccatgg cgttcccgct gctgggattc     540
163 tacctgcccc tggccgtggt ggtcttctgc tccctgaagg tggtgactgc cctggcccag     600
165 aggccaccca ccgacgtggg gcaggcagag gccacccgca aggctgcccg catggtctgg     660
167 gccaacctcc tggtgttcgt ggtctgcttc ctgcccctgc acgtggggct gacagtgcgc     720
169 ctcgcagtgg gctggaacgc ctgtgccctc ctggagacga tccgtcgcgc cctgtacata     780
171 accagcaagc tctcagatgc caactgctgc ctggacgcca tctgctacta ctacatggcc     840
```

```
173 aaggagttcc aggaggcgtc tgcactggcc gtggctccca gtgctaaggc ccacaaaagc    900
175 caggactctc tgtgcgtgac cctcgcctaa.                                     930
178 <210> SEQ ID NO: 4
179 <211> LENGTH: 309
180 <212> TYPE: PRT
181 <213> ORGANISM: human
183 <400> SEQUENCE: 4
185 Met Asn Gly Thr Tyr Asn Thr Cys Gly Ser Ser Asp Leu Thr Trp Pro
186 1               5                   10                  15
189 Pro Ala Ile Lys Leu Gly Phe Tyr Ala Tyr Leu Gly Val Leu Leu Val
190             20                  25                  30
193 Leu Gly Leu Leu Leu Asn Ser Leu Ala Leu Trp Val Phe Cys Cys Arg
194         35                  40                  45
197 Met Gln Gln Trp Thr Glu Thr Arg Ile Tyr Met Thr Asn Leu Ala Val
198     50                  55                  60
201 Ala Asp Leu Cys Leu Leu Cys Thr Leu Pro Phe Val Leu His Ser Leu
202 65                  70                  75                  80
205 Arg Asp Thr Ser Asp Thr Pro Leu Cys Gln Leu Ser Gln Gly Ile Tyr
206             85                  90                  95
209 Leu Thr Asn Arg Tyr Met Ser Ile Ser Leu Val Met Ala Ile Ala Val
210             100                 105                 110
213 Asp Arg Tyr Val Ala Val Arg His Pro Leu Arg Ala Arg Gly Leu Arg
214         115                 120                 125
217 Ser Pro Arg Gln Ala Ala Ala Val Cys Ala Val Leu Trp Val Leu Val
218     130                 135                 140
221 Ile Gly Ser Leu Val Ala Arg Trp Leu Leu Gly Ile Gln Glu Gly Gly
222 145                 150                 155                 160
225 Phe Cys Phe Arg Ser Thr Arg His Asn Phe Asn Ser Met Ala Phe Pro
226                 165                 170                 175
229 Leu Leu Gly Phe Tyr Leu Pro Leu Ala Val Val Val Phe Cys Ser Leu
230             180                 185                 190
233 Lys Val Val Thr Ala Leu Ala Gln Arg Pro Pro Thr Asp Val Gly Gln
234         195                 200                 205
237 Ala Glu Ala Thr Arg Lys Ala Ala Arg Met Val Trp Ala Asn Leu Leu
238     210                 215                 220
241 Val Phe Val Val Cys Phe Leu Pro Leu His Val Gly Leu Thr Val Arg
242 225                 230                 235                 240
245 Leu Ala Val Gly Trp Asn Ala Cys Ala Leu Leu Glu Thr Ile Arg Arg
246                 245                 250                 255
249 Ala Leu Tyr Ile Thr Ser Lys Leu Ser Asp Ala Asn Cys Cys Leu Asp
250             260                 265                 270
253 Ala Ile Cys Tyr Tyr Tyr Met Ala Lys Glu Phe Gln Glu Ala Ser Ala
254         275                 280                 285
257 Leu Ala Val Ala Pro Ser Ala Lys Ala His Lys Ser Gln Asp Ser Leu
258     290                 295                 300
261 Cys Val Thr Leu Ala
262 305
265 <210> SEQ ID NO: 5
266 <211> LENGTH: 924
```

```
267 <212> TYPE: DNA
268 <213> ORGANISM: mouse
270 <400> SEQUENCE: 5
271 atgaatagta caacctgtaa cagcaccctc acgtggcctg cttccgtcaa caacttcttc      60
273 atcatctact cagccttgct gctggtgctg ggcctgctgc tcaacagcgt ggcactctgg     120
275 gtattctgct atcgcatgca ccagtggaca gagacccgca tctatatgac caacctggct     180
277 gtggccgacc tctgcctgct ctgctccttg ccatttgtgc tgtactccct gaaatatagt     240
279 tcttcagaca cacccgtctg ccagctctca cagggcatct acctggccaa cagatacatg     300
281 agcataagcc tggtcactgc cattgctgtg gaccgctatg tggcagtgcg gcatcccctg     360
283 cgtgcgcgtg agctgcggtc cccgagacag gctgcagcag tgtgtgtggc cctttgggtg     420
285 atagtggtca cctccctggt agtgcgctgg cgcctgggga tgcaggaggg tggcttctgc     480
287 ttcagcagcc aaacccggcg caatttcagc accactgcct tctcactgct gggattctac     540
289 ctgccgctgg ccatcgtggt cttctgctct ttgcaggtag tgactgtgct atcgagaagg     600
291 ccagccgctg atgtggggca ggcagaggcc acccaaaagg ccacccacat ggtctgggcc     660
293 aacttggctg tgtttgtcat ctgcttcctg cccttgcatg tggtcctgac cgtgcaggtc     720
295 tccctgaacc tcaatacctg tgctgcccga cacaccttca gccgtgccct gtccatcaca     780
297 ggtaaactct cagacaccaa ctgctgcctg gatgccatct gttactacta catggccaga     840
299 gagttccagg aagcgtccaa gccagccacg tcttccaaca caccccacaa gagccaagat     900
301 tcccagatcc tgagcctcac ctag                                            924
304 <210> SEQ ID NO: 6
305 <211> LENGTH: 307
306 <212> TYPE: PRT
307 <213> ORGANISM: mouse
309 <400> SEQUENCE: 6
311 Met Asn Ser Thr Thr Cys Asn Ser Thr Leu Thr Trp Pro Ala Ser Val
312 1               5                   10                  15
315 Asn Asn Phe Phe Ile Ile Tyr Ser Ala Leu Leu Leu Val Leu Gly Leu
316             20                  25                  30
319 Leu Leu Asn Ser Val Ala Leu Trp Val Phe Cys Tyr Arg Met His Gln
320         35                  40                  45
323 Trp Thr Glu Thr Arg Ile Tyr Met Thr Asn Leu Ala Val Ala Asp Leu
324     50                  55                  60
327 Cys Leu Leu Cys Ser Leu Pro Phe Val Leu Tyr Ser Leu Lys Tyr Ser
328 65                  70                  75                  80
331 Ser Ser Asp Thr Pro Val Cys Gln Leu Ser Gln Gly Ile Tyr Leu Ala
332                 85                  90                  95
335 Asn Arg Tyr Met Ser Ile Ser Leu Val Thr Ala Ile Ala Val Asp Arg
336             100                 105                 110
339 Tyr Val Ala Val Arg His Pro Leu Arg Ala Arg Glu Leu Arg Ser Pro
340         115                 120                 125
343 Arg Gln Ala Ala Ala Val Cys Val Ala Leu Trp Val Ile Val Val Thr
344     130                 135                 140
347 Ser Leu Val Val Arg Trp Arg Leu Gly Met Gln Glu Gly Gly Phe Cys
348 145                 150                 155                 160
351 Phe Ser Ser Gln Thr Arg Arg Asn Phe Ser Thr Thr Ala Phe Ser Leu
352                 165                 170                 175
355 Leu Gly Phe Tyr Leu Pro Leu Ala Ile Val Val Phe Cys Ser Leu Gln
356             180                 185                 190
359 Val Val Thr Val Leu Ser Arg Arg Pro Ala Ala Asp Val Gly Gln Ala
```

RAW SEQUENCE LISTING   DATE: 09/05/2006
PATENT APPLICATION: US/10/590,953   TIME: 15:07:20

Input Set : E:\PC32099A_SEQUENCE LISTING.txt
Output Set: N:\CRF4\09052006\J590953.raw

```
360           195              200              205
363 Glu Ala Thr Gln Lys Ala Thr His Met Val Trp Ala Asn Leu Ala Val
364       210              215              220
367 Phe Val Ile Cys Phe Leu Pro Leu His Val Val Leu Thr Val Gln Val
368 225              230              235              240
371 Ser Leu Asn Leu Asn Thr Cys Ala Ala Arg Asp Thr Phe Ser Arg Ala
372               245              250              255
375 Leu Ser Ile Thr Gly Lys Leu Ser Asp Thr Asn Cys Cys Leu Asp Ala
376           260              265              270
379 Ile Cys Tyr Tyr Tyr Met Ala Arg Glu Phe Gln Glu Ala Ser Lys Pro
380           275              280              285
383 Ala Thr Ser Ser Asn Thr Pro His Lys Ser Gln Asp Ser Gln Ile Leu
384       290              295              300
387 Ser Leu Thr
388 305
391 <210> SEQ ID NO: 7
392 <211> LENGTH: 61
393 <212> TYPE: DNA
394 <213> ORGANISM: Artificial Sequence
396 <220> FEATURE:
397 <223> OTHER INFORMATION: primer
399 <400> SEQUENCE: 7
400 ccggaattcg ccaccatgga ttacaaggat gacgacgata agaatggcac ctacaacacc     60
402 t                                                                     61
405 <210> SEQ ID NO: 8
406 <211> LENGTH: 30
407 <212> TYPE: DNA
408 <213> ORGANISM: Artificial Sequence
410 <220> FEATURE:
411 <223> OTHER INFORMATION: primer
413 <400> SEQUENCE: 8
414 tcgtctagaa ttaggcgagg gtcacgcaca                                       30
417 <210> SEQ ID NO: 9
418 <211> LENGTH: 36
419 <212> TYPE: DNA
420 <213> ORGANISM: Artificial Sequence
422 <220> FEATURE:
423 <223> OTHER INFORMATION: primer
425 <400> SEQUENCE: 9
426 ccggaattcg ccaccatgaa tggcacctac aacacc                                36
429 <210> SEQ ID NO: 10
430 <211> LENGTH: 40
431 <212> TYPE: DNA
432 <213> ORGANISM: Artificial Sequence
434 <220> FEATURE:
435 <223> OTHER INFORMATION: primer
437 <400> SEQUENCE: 10
438 ccccgaattc gccaccatga atagtacaac ctgtaacagc                            40
441 <210> SEQ ID NO: 11
```

VERIFICATION SUMMARY   DATE: 09/05/2006
PATENT APPLICATION: US/10/590,953   TIME: 15:07:21

Input Set : **E:\PC32099A_SEQUENCE LISTING.txt**
Output Set: **N:\CRF4\09052006\J590953.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date